#8

SEQUENCE LISTING

<110>   Kinney, Anthony

<120>   Hypoallergenic Transgenic Soybeans

<130>   BB1432 US NA

<140>   US/09/805,694
<141>   2001-03-14

<150>   60/189,823
<151>   2000-03-16

<160>   16

<170>   Microsoft Office 97

<210>   1
<211>   1156
<212>   DNA
<213>   chimeric construct

<400>   1
```
gcggccgcat gggtttcctt gtgttgcttc ttttctccct cttaggtctc tcttctagtt     60
ccagcatatc aactcatcgt tccatattgg accttgacct aaccaagttt accacacaga    120
aacaggtgtc ttcactgttc caactatgga agagtgagca tggacgtgtc taccataacc    180
acgaagaaga ggcaaagaga cttgagattt tcaagaataa ctcgaactat atcagggaca    240
tgaatgcaaa cagaaaatca ccccattctc atcgtttagg attgaacaag tttgctgaca    300
tcactcctca agagttcagc aaaaagtact tgcaagctcc caaggatgtg tcgcagcaaa    360
tcaaaatggc caacaagaaa atgaagaagg aacaatattc ttgtgaccat ccacctgcat    420
catgggattg gaggaaaaaa ggtgtcatca cccagtaaaa gtaccaaggg ggctgtggaa    480
ggggttgggc gttttctgcc acgggagcca tagaagcagc acatgcaata gcaacaggag    540
accttgttag cctttctgaa caagaactcg tagactgtgt ggaagaaagc gaaggttctt    600
acaatggatg gcagtatcaa tcgttcgaat gggtttttaga acatggtggc attgccactg    660
atgatgatta tccttacaga gctaaagagg gtagatgcaa agccaataag atacaagaca    720
aggttacaat tgacggatat gaaactctaa taatgtcaga tgagagtaca gaatcagaga    780
cagagcaagc gttcttaagc gccatccttg agcaaccaat tagtgtctca attgatgcaa    840
aagattttca tttatacacc gggggaattt atgatggaga aaactgtaca agtccgtatg    900
ggattaatca ctttgtttta cttgtgggtt atggttcagc ggatggtgta gattactgga    960
tagcgaaaaa ttcatgggga gaagattggg gagaagatgg ttacatttgg atccaaagaa   1020
acacgggtaa tttattagga gtgtgtggga tgaattattt cgcttcatac ccaaccaaag   1080
aggaatcaga aacactggtg tctgctcgcg ttaaaggtca tcgaagagtt gatcactctc   1140
ctctttgagc ggccgc                                                   1156
```

<210>   2
<211>   2970
<212>   DNA
<213>   chimeric construct

<400>   2
```
aagcttgatc catgcccttc atttgccgct attaattaat ttggtaacag tagtccgtac     60
taatcagtta cttatccttc ctccatcata attaatcttg gtagtctcga atgccacaac    120
actgactagt ctcttggatc ataagaaaaa gccaaggaac aaaagaagac aaaacacaat    180
gagagtatcc tttgcatagc aatgtctaag ttcataaaat tcaaacaaaa acgcaatcac    240
acacagtgga catcacttat ccactagctg aatcaggatc gccgcgtcaa gaaaaaaaaa    300
ctggacccca aaagccatgc acaacaacac gtactacaa aggtgtcaat cgagcagccc    360
aaaacattca ccaactcaac ccatcatgag ccctcacatt tgttgtttct aacccaacct    420
caaactcgta ttctcttccg ccacctcatt tttgtttatt tcaacacccg tcaaactgca    480
tgccacccg tggccaaatg tccatgcatg ttaacaagac ctatgactat aaatatctgc    540
```

```
aatctcggcc caggtttttca tcatcaagaa ccagttcaat atcctagtac accgtattaa    600
agaatttaag atatactaac agcggccgca tgggtttcct tgtgttgctt ctttctcccc    660
tcttaggtct ctcttctagt tccagcatat caactcatcg ttccatattg gaccttgacc    720
taaccaagtt taccacacag aaacaggtgt cttcactgtt ccaactatgg aagagtgagc    780
atggacgtgt ctaccataac cacgaagaag aggcaaagag acttgagatt ttcaagaata    840
actcgaacta tatcagggac atgaatgcaa acagaaaatc accccattct catcgtttag    900
gattgaacaa gtttgctgac atcactcctc aagagttcag caaaaagtac ttgcaagctc    960
ccaaggatgt gtcgcagcaa atcaaaatgg ccaacaagaa aatgaagaag gaacaatatt   1020
cttgtgacca tccacctgca tcatgggatt ggaggaaaaa aggtgtcatc acccaagtaa   1080
agtaccaagg gggctgtgga aggggttggg cgttttctgc cacgggagcc atagaagcag   1140
cacatgcaat agcaacagga gaccttgtta gcctttctga caagaactc gtagactgtg    1200
tggaagaaag cgaaggttct tacaatggat ggcagtatca atcgttcgaa tgggttttag   1260
aacatggtgg cattgccact gatgatgatt atccttacag agctaaagag ggtagatgca   1320
aagccaataa gatacaagac aaggttacaa ttgacggata tgaaactcta ataatgtcag   1380
atgagagtac agaatcagag acagagcaag cgttcttaag cgccatcctt gagcaaccaa   1440
ttagtgtctc aattgatgca aaagattttc atttatacac cgggggaatt tatgatggag   1500
aaaactgtac aagtccgtat gggattaatc actttgtttt acttgtgggt tatggttcag   1560
cggatggtgt agattactgg atagcgaaaa attcatgggg agaagattgg ggagaagatg   1620
gttacatttg gatccaaaga aacacgggta atttattagg agtgtgtggg atgaattatt   1680
tcgcttcata cccaaccaaa gaggaatcag aaacactggt gtctgctcgc gttaaaggtc   1740
atcgaagagt tgatcactct cctctttgag cggccgctac atggccacgt gcatgaagta   1800
tgaactaaaa tgcatgtagg tgtaagagct catggagagc atggaatatt gtatccgacc   1860
atgtaacagt ataataactg agctccatct cacttcttct atgaataaac aaaggatgtt   1920
atgatatatt aacactctat ctatgcacct tattgttcta tgataaattt cctcttatta   1980
ttataaatca tctgaatcgt gacggcttat ggaatgcttc aaatagtaca aaaacaaatg   2040
tgtactataa gactttctaa acaattctaa ctttagcatt gtgaacgaga cataagtgtt   2100
aagaagacat aacaattata atggaagaag tttgtctcca tttatatatt atatattacc   2160
cactatgta ttatattagg atgttaagga gacataacaa ttataaagag agaagtttgt    2220
atccatttat atattatata ctacccattt atatattata cttatccact tatttaatgt   2280
ctttataagg tttgatccat gatatttcta atatttttagt tgatatgtat atgaaagggt   2340
actatttgaa ctctcttact ctgtataaag gttggatcat ccttaaagtg ggtctattta   2400
attttattgc ttcttacaga taaaaaaaaa attatgagtt ggtttgataa aatattgaag   2460
gatttaaaat aataataaat aataaataac atataatata tgtatataaa tttattataa   2520
tataacattt atctataaaa aagtaaatat tgtcataaat ctatacaatc gtttagcctt   2580
gctggacgac tctcaattat ttaaacgaga gtaaacatat ttgacttttt ggttatttaa   2640
caaattatta tttaacacta tatgaaattt ttttttttta tcagcaaaga aataaaatta   2700
aattaagaag acaatggtg tgtcccaatc cttatacaac caacttccac aagaaagtca    2760
agtcagagac aacaaaaaaa caagcaaagg aaattttta atttgagttg tcttgtttgc    2820
tgcataattt atgcagtaaa acactacaca taacccttt agcagtagag caatggttga    2880
ccgtgtgctt agcttctttt attttattt tttatcagca aagaataaat aaaataaaat    2940
gagacacttc agggatgttt caacaagctt                                    2970

<210>    3
<211>    1600
<212>    DNA
<213>    Glycine max

<400>    3
ggggaaacaa aactacccct ttgcttttgc tctttgttct ttgtcatgga gtggccacaa     60
caacaatggc cttccgtgat gatgagggtg gtgataaaaa gtcaccaaaa agtttgtttt    120
tgatgagcaa ctccacgagg gttttcaaga ctgatgcagg gaaatgcgt gtgctgaaaa     180
gccatggtgg taggatattt tataggcaca tgcacattgg cttcatctct atggaaccaa    240
agtccttgtt tgttcctcag tacctcgact ccaatctcat catattcatc cgtagagggg    300
aagcaaagct gggattcata tatgatgatg aactagcgga aaggagattg aagacagggg    360
acttgtacat gattccatct ggttcagcat tctatttggt gaacatagga gaaggtcaga    420
gacttcacgt tatctgcagc attgacccct ctacaagctt gggattagag accttccagt    480
ccttctatat tggggggagga gccaattcgc actcggtgct ttctggattc gaacctgcca    540
tccttgaaac tgcatttaat gaatcaagaa cggtggtaga ggaaatcttc tccaaggaac    600
tagatgggcc aattatgttc gtggatgatt ctcatgcacc tagcttatgg actaaattcc    660
ttcaactgaa gaaggatgac aaagagcaac agctgaagaa aatgatgcaa gaccaagagg    720
```

```
aggatgagga ggagaagcaa acaagtaggt catggaggaa gctcttggaa accgtatttg  780
ggaaggtgaa tgagaagata gagaacaaag acactgctgg ttcccctgcc tcttacaacc  840
tctacgatga caaaaaagcc gatttcaaaa acgcttatgg ttggagcaag gcactgcatg  900
gaggcgagta tcctccactc agcgaaccgg atattggagt tttacttgtc aaactctcag  960
cgggatccat gttggcacct catgtgaatc caatatcaga tgagtatacc atagtgctga 1020
gtggttatgg tgaactgcat atagggtatc caaacggaag caaagcaatg aaaactaaaa 1080
tcaaacaagg ggacgtgttt gttgtgccaa gatacttccc cttctgtcaa gtagcatcaa 1140
gggatggacc cttagagttc tttggcttct ccacttctgc aaggaagaac aagccacagt 1200
ttctggctgg tgctgcgtcc cttctaagga ccttgatggg gccggagctt tcggcggcgt 1260
tcggagtgag cgaggacacg ttgcggcgcg ctgttgatgc tcagcatgag gctgtgatac 1320
tgccatcagc atgggctgca ccaccggaaa atgcagggaa gctgaagatg gaagaagagc 1380
caaatgctat tagaagcttt gccaatgatg tggttatgga tgttttttaa tttgaacact 1440
tgatttggaa tagggggttat ttggtagtgc tagtgcctag tggaattctg tgttgagttt 1500
tttgttcttt atatttagtt gagatgtgtg ttgtgttctt gagttgtgaa taaaaatcta 1560
ctttctttgt gcarraaaaa aaaaaaaaaa aaaaaaaaaa                        1600
```

```
<210>  4
<211>  454
<212>  PRT
<213>  Glycine max

<400>  4
Met ala Phe Arg Asp Asp Glu Gly Gly Asp Lys Lys Ser Pro Lys Ser
 1               5                  10                  15

Leu Phe Leu Met Ser Asn Ser Thr Arg Val Phe Lys Thr Asp Ala Gly
            20                  25                  30

Glu Met Arg Val Leu Lys Ser His Gly Gly Arg Ile Phe Tyr Arg His
        35                  40                  45

Met His Ile Gly Phe Ile Ser Met Glu Pro Lys Ser Leu Phe Val Pro
    50                  55                  60

Gln Tyr Leu Asp Ser Asn Leu Ile Ile Phe Ile Arg Arg Gly Glu Ala
65                  70                  75                  80

Lys Leu Gly Phe Ile Tyr Asp Asp Glu Leu Ala Glu Arg Arg Leu Lys
                85                  90                  95

Thr Gly Asp Leu Tyr Met Ile Pro Ser Gly Ser Ala Phe Tyr Leu Val
            100                 105                 110

Asn Ile Gly Glu Gly Gln Arg Leu His Val Ile Cys Ser Ile Asp Pro
        115                 120                 125

Ser Thr Ser Leu Gly Leu Glu Thr Phe Gln Ser Phe Tyr Ile Gly Gly
    130                 135                 140

Gly Ala Asn Ser His Ser Val Leu Ser Gly Phe Glu Pro Ala Ile Leu
145                 150                 155                 160

Glu Thr Ala Phe Asn Glu Ser Arg Thr Val Val Glu Glu Ile Phe Ser
                165                 170                 175

Lys Glu Leu Asp Gly Pro Ile Met Phe Val Asp Asp Ser His Ala Pro
            180                 185                 190

Ser Leu Trp Thr Lys Phe Leu Gln Leu Lys Lys Asp Asp Lys Glu Gln
            195                 200                 205
```

```
Gln Leu Lys Lys Met Met Gln Asp Gln Glu Glu Asp Glu Glu Glu Lys
    210             215             220
Gln Thr Ser Arg Ser Trp Arg Lys Leu Leu Glu Thr Val Phe Gly Lys
225             230             235             240
Val Asn Glu Lys Ile Glu Asn Lys Asp Thr Ala Gly Ser Pro Ala Ser
            245             250             255
Tyr Asn Leu Tyr Asp Asp Lys Lys Ala Asp Phe Lys Asn Ala Tyr Gly
            260             265             270
Trp Ser Lys Ala Leu His Gly Gly Glu Tyr Pro Pro Leu Ser Glu Pro
        275             280             285
Asp Ile Gly Val Leu Leu Val Lys Leu Ser Ala Gly Ser Met Leu Ala
    290             295             300
Pro His Val Asn Pro Ile Ser Asp Glu Tyr Thr Ile Val Leu Ser Gly
305             310             315             320
Tyr Gly Glu Leu His Ile Gly Tyr Pro Asn Gly Ser Lys Ala Met Lys
            325             330             335
Thr Lys Ile Lys Gln Gly Asp Val Phe Val Val Pro Arg Tyr Phe Pro
        340             345             350
Phe Cys Gln Val Ala Ser Arg Asp Gly Pro Leu Glu Phe Phe Gly Phe
        355             360             365
Ser Thr Ser Ala Arg Lys Asn Lys Pro Gln Phe Leu Ala Gly Ala Ala
    370             375             380
Ser Leu Leu Arg Thr Leu Met Gly Pro Glu Leu Ser Ala Ala Phe Gly
385             390             395             400
Val Ser Glu Asp Thr Leu Arg Arg Ala Val Asp Ala Gln His Glu Ala
            405             410             415
Val Ile Leu Pro Ser Ala Trp Ala Ala Pro Pro Glu Asn Ala Gly Lys
            420             425             430
Leu Lys Met Glu Glu Glu Pro Asn Ala Ile Arg Ser Phe Ala Asn Asp
        435             440             445
Val Val Met Asp Val Phe
    450

<210>    5
<211>    494
<212>    DNA
<213>    Glycine max

<220>
<221> unsure
<222> (9)
<223> n = A, C, G, or T

<220>
```

```
<221> unsure
<222> (388)
<223> n = A, C, G, or T

<220>
<221> unsure
<222> (392)..(393)
<223> n = A, C, G, or T

<220>
<221> unsure
<222> (460)
<223> n = A, C, G, or T

<220>
<221> unsure
<222> (463)
<223> n = A, C, G, or T

<220>
<221> unsure
<222> (468)
<223> n = A, C, G, or T

<400>   5
acacagctng cacatattac atacacgtga atcactaatt aagccatgga gaagaaatca  60
atagctgggt tgtgcttcct cttccttgtt ctctttgttg ctcaagaagt tgtggtgcaa  120
actgaggcaa agacttgcga gaacctggct gatacataca ggggtccatg cttcaccact  180
ggcagctgcg atgatcactg caagaacaaa gagcacttgc tcagaggcag atgcagggac  240
gattttcgct gttggtgcac caaaaactgt taaatggatc cattcactcc aacgtgaaga  300
agatgcatgc agcgctattt tataaaaaat acaactacta tatactatat ataataagac  360
tgggcgctgc atcaatgacc ctatgtanta tnntatatat tattaccgat gtcaagaact  420
atagatgcat gtactgtgca taacggctga gttatgtccn tangttanga ataaaaataa  480
agtgctgttg ttgc                                                    494
```

```
<210>   6
<211>   75
<212>   PRT
<213>   Glycine max
```

```
<400>   6
Met Glu Lys Lys Ser Ile Ala Gly Leu Cys Phe Leu Phe Leu Val Leu
 1               5                  10                  15

Phe Val Ala Gln Glu Val Val Val Gln Thr Glu Ala Lys Thr Cys Glu
            20                  25                  30

Asn Leu Ala Asp Thr Tyr Arg Gly Pro Cys Phe Thr Thr Gly Ser Cys
        35                  40                  45

Asp Asp His Cys Lys Asn Lys Glu His Leu Leu Arg Gly Arg Cys Arg
    50                  55                  60

Asp Asp Phe Arg Cys Trp Cys Thr Lys Asn Cys
65                  70                  75
```

```
<210>   7
<211>   30
<212>   DNA
<213>   Artificial Sequence
```

<220>
<223>   Description of Artificial Sequence: P34 gene primer

<400>   7
gaattcgcgg ccgcatgggt ttccttgtgt   30

<210>   8
<211>   30
<212>   DNA
<213>   Glycine max

<220>
<223>   Description of Artificial Sequence: P34 gene primer

<400>   8
gaattcgcgg ccgctcaaag aggagagtga   30

<210>   9
<211>   701
<212>   DNA
<213>   Glycine max

<400>   9
ttaagctttc aagagacaaa ctgctttgaa aaatgggatc caaggttgtt gcatccgttg   60
cccttctcct ctccatcaac attctttttca tttccatggt tagctccagc agccactacg 120
atccacagcc ccaaccttct cacgtcactg ctcttattac acgacctagt tgtccggatc 180
tgagtatttg cctcaatatt ttaggcgggt ctctaggaac cgtggatgat tgttgtgccc 240
tcatcggtgg tcttggtgac attgaagcca ttgtgtgcct ttgcatccaa ctcagggccc 300
tcggaatatt aaaccttaac cgtaatttgc agttaatatt aaactcctgt ggacgaagct 360
acccgtcaaa cgccacttgc ccccgaacct aagaacagaa tatgtatggc actaattacc 420
atattacttc gtatcatggt gtttgtttgt ttgtctgtgt ttaaagttaa ggatgttata 480
cccttcgtgc ctgctacata tatatagtgg gcactataat attaccaata aattaacgtc 540
catatataag aataataata aataaataaa tatttctata caaataaagg ttacgtaatg 600
ttgttgttct cgtggatggg gatcttatct tcctcctcgc tatctttgtt tatcgtattt 660
cagtgaaagt tgttcaataa aagtcctttg ttcaacaagt g   701

<210>   10
<211>   119
<212>   PRT
<213>   Glycine max

<400>   10
Met Gly Ser Lys Val Val Ala Ser Val Ala Leu Leu Leu Ser Ile Asn
 1   5   10   15

Ile Leu Phe Ile Ser Met Val Ser Ser Ser Ser His Tyr Asp Pro Gln
            20   25   30

Pro Gln Pro Ser His Val Thr Ala Leu Ile Thr Arg Pro Ser Cys Pro
        35   40   45

Asp Leu Ser Ile Cys Leu Asn Ile Leu Gly Gly Ser Leu Gly Thr Val
    50   55   60

Asp Asp Cys Cys Ala Leu Ile Gly Gly Leu Gly Asp Ile Glu Ala Ile
65   70   75   80

Val Cys Leu Cys Ile Gln Leu Arg Ala Leu Gly Ile Leu Asn Leu Asn
                85   90   95

Arg Asn Leu Gln Leu Ile Leu Asn Ser Cys Gly Arg Ser Tyr Pro Ser
        100   105   110

Asn Ala Thr Cys Pro Arg Thr
        115

<210>   11
<211>   396
<212>   DNA
<213>   Glycine max

<400>   11
atgtcgtggc aagcttatgt cgacgatcac cttctgtgtg gcatcgaagg taaccacctc   60
actcacgctg ctatcatcgg ccaagacggc agcgtttggc ttcagagtac cgacttccct 120
cagttcaaac ctgaggagat aactgccatc atgaatgact ttaatgagcc tggatcactt 180
gctccaactg gattgtatct cggtggcacc aaatatatgg tcatccaggg tgaacccggt 240
gctgtcattc gagggaagaa gggtcctggt ggtgttactg tgaagaagac cggtgcggcc 300
ttgatcattg gcatttatga tgaaccaatg actccaggtc aatgcaacat ggtagttgaa 360
aggcttggtg attacctcat agatcaaggc tactga   396

<210>   12
<211>   131
<212>   PRT
<213>   Glycine max

<400>   12
Met Ser Trp Gln Ala Tyr Val Asp Asp His Leu Leu Cys Gly Ile Glu
  1   5   10   15

Gly Asn His Leu Thr His Ala Ala Ile Ile Gly Gln Asp Gly Ser Val
            20   25   30

Trp Leu Gln Ser Thr Asp Phe Pro Gln Phe Lys Pro Glu Glu Ile Thr
        35   40   45

Ala Ile Met Asn Asp Phe Asn Glu Pro Gly Ser Leu Ala Pro Thr Gly
    50   55   60

Leu Tyr Leu Gly Gly Thr Lys Tyr Met Val Ile Gln Gly Glu Pro Gly
65   70   75   80

Ala Val Ile Arg Gly Lys Lys Gly Pro Gly Gly Val Thr Val Lys Lys
                85   90   95

Thr Gly Ala Ala Leu Ile Ile Gly Ile Tyr Asp Glu Pro Met Thr Pro
            100   105   110

Gly Gln Cys Asn Met Val Val Glu Arg Leu Gly Asp Tyr Leu Ile Asp
            115   120   125

Gln Gly Tyr
    130

<210>   13
<211>   396
<212>   DNA
<213>   Glycine max

<400>   13

```
atgtcctggc aggcgtatgt cgacgatcac cttctgtgtg acatcgaagg taaccacctc  60
actcacgctg ctatcatcgg ccaagacggc agcgtttggg ctcagagtac cgacttccct 120
cagttcaaac ctgaggagat aactgccatc atgaatgact ttaatgagcc tggatcactt 180
gctccaactg gattgtatct cggtggcacc aaatatatgg tcatccaggg tgaacccggt 240
gctgtcattc gagggaagaa gggtcctggt ggtgttactg tgaagaagac cggtgcggcc 300
ttgatcattg gcatttatga tgaaccaatg actccaggtc aatgcaacat ggtagttgaa 360
aggcctggtg attacctcat cgaccagggc tactga                          396
```

```
<210>   14
<211>   131
<212>   PRT
<213>   Glycine max

<400>   14
```

```
Met Ser Trp Gln Ala Tyr Val Asp Asp His Leu Leu Cys Asp Ile Glu
  1               5                  10                  15

Gly Asn His Leu Thr His Ala Ala Ile Ile Gly Gln Asp Gly Ser Val
             20                  25                  30

Trp Ala Gln Ser Thr Asp Phe Pro Gln Phe Lys Pro Glu Glu Ile Thr
         35                  40                  45

Ala Ile Met Asn Asp Phe Asn Glu Pro Gly Ser Leu Ala Pro Thr Gly
     50                  55                  60

Leu Tyr Leu Gly Gly Thr Lys Tyr Met Val Ile Gln Gly Glu Pro Gly
 65                  70                  75                  80

Ala Val Ile Arg Gly Lys Lys Gly Pro Gly Gly Val Thr Val Lys Lys
                 85                  90                  95

Thr Gly Ala Ala Leu Ile Ile Gly Ile Tyr Asp Glu Pro Met Thr Pro
             100                 105                 110

Gly Gln Cys Asn Met Val Val Glu Arg Pro Gly Asp Tyr Leu Ile Asp
         115                 120                 125

Gln Gly Tyr
     130
```

```
<210>   15
<211>   1746
<212>   DNA
<213>   Glycine max

<400>   15
aaaacaactc aaacattctc tccattggtc cttaaacact catcagtcat caccatggcc  60
aagctagttt tttccctttg ttttctgctt ttcagtggct gctgcttcgc tttcagttcc 120
agagagcagc ctcagcaaaa cgagtgccag atccaaaaac tcaatgccct caaaccgggt 180
aaccgtatag agtcagaagg agggctcatt gagacatgga accctaacaa caagccattc 240
cagtgtgccg gtgttgccct ctctcgctgc accctcaacc gcaacgccct tcgtagacct 300
tcctacacca acggtcccca agaaatctac atccaacaag gtaagggtat ttttggcatg 360
atatacccgg gttgttctag cacatttgaa gagcctcaac aacctcaaca agaggacaa 420
agcagcagac cacaagaccg tcaccagaag atctataact ccagagaggg tgatttgatc 480
gcagtgccta ctggtgttgc atggtggatg tacaacaatg aagacactcc tgttgttgcc 540
gtttctatta ttgacaccaa cagcttggag aaccagctcg accagatgcc taggagattc 600
tatcttgctg ggaaccaaga gcaagagttt ctaaaatatc agcaagagca aggaggtcat 660
caaagccaga aaggaaagca tcagcaagaa gaagaaaacg aaggaggcag catattgagt 720
ggcttcaccc tggaattctt ggaacatgca ttcagcgtgg acaagcagat agcgaaaaac 780
```

```
ctacaaggag agaacgaagg ggaagacaag ggagccattg tgacagtgaa aggaggtctg    840
agcgtgataa aaccacccac ggacgagcag caacaaagac cccaggaaga ggaagaagaa    900
gaagaggatg agaagccaca gtgcaagggt aaagacaaac actgccaacg cccccgagga    960
agccaaagca aaagcagaag aaatggcatt gacgagacca tatgcaccat gagacttcgc   1020
cacaacattg ccagacttc atcacctgac atctacaacc ctcaagccgg tagcgtcaca   1080
accgccacca gccttgactt cccagccctc tcgtggctca gactcagtgc tggatttggg   1140
tctctccgca agaatgcaat gttcgtgcca cactacaacc tgaacgcgaa cagcataata   1200
tacgcattga atggacgggc attgatacaa gtggtgaatt gcaacggtga gagagtgttt   1260
gatggagagc tgcaagaggg acgggtgctg atcgtgccac aaaactttgt ggtggctgca   1320
agatcacaga gtgacaactt cgagtatgtg tcattcaaga ccaatgatac acccatgatc   1380
ggcactcttg caggggcaaa ctcattgttg aacgcattac cagaggaagt gattcagcac   1440
actttcaacc taaaaagcca gcaggccagg cagataaaga caacaacccc tttcaagttc   1500
ctggttccac ctcaggagtc tcagaagaga gctgtggctt agagcccttt ttgtatgtgc   1560
taccccactt ttgtcttttt ggcaatagtg ctagcaacca ataaataata ataataataa   1620
tgaataagaa aacaaaggct ttagcttgcc ttttgttcac tgtaaaataa taatgtaagt   1680
actctctata atgagtcacg aaactttgc gggaataaaa ggagaaattc caatgagttt   1740
tctgtt                                                              1746


<210>  16
<211>  495
<212>  PRT
<213>  Glycine max

<400>  16
Met Ala Lys Leu Val Phe Ser Leu Cys Phe Leu Leu Phe Ser Gly Cys
  1               5                  10                  15

Cys Phe Ala Phe Ser Ser Arg Glu Gln Pro Gln Gln Asn Glu Cys Gln
               20                  25                  30

Ile Gln Lys Leu Asn Ala Leu Lys Pro Gly Asn Arg Ile Glu Ser Glu
           35                  40                  45

Gly Gly Leu Ile Glu Thr Trp Asn Pro Asn Asn Lys Pro Phe Gln Cys
       50                  55                  60

Ala Gly Val Ala Leu Ser Arg Cys Thr Leu Asn Arg Asn Ala Leu Arg
 65                  70                  75                  80

Arg Pro Ser Tyr Thr Asn Gly Pro Gln Glu Ile Tyr Ile Gln Gln Gly
               85                  90                  95

Lys Gly Ile Phe Gly Met Ile Tyr Pro Gly Cys Ser Ser Thr Phe Glu
              100                 105                 110

Glu Pro Gln Gln Pro Gln Gln Arg Gly Gln Ser Ser Arg Pro Gln Asp
          115                 120                 125

Arg His Gln Lys Ile Tyr Asn Ser Arg Glu Gly Asp Leu Ile Ala Val
          130                 135                 140

Pro Thr Gly Val Ala Trp Trp Met Tyr Asn Asn Glu Asp Thr Pro Val
145                 150                 155                 160

Val Ala Val Ser Ile Ile Asp Thr Asn Ser Leu Glu Asn Gln Leu Asp
              165                 170                 175

Gln Met Pro Arg Arg Phe Tyr Leu Ala Gly Asn Gln Glu Gln Glu Phe
          180                 185                 190
```

```
Leu Lys Tyr Gln Gln Glu Gln Gly Gly His Gln Ser Gln Lys Gly Lys
        195             200             205

His Gln Gln Glu Glu Glu Asn Glu Gly Gly Ser Ile Leu Ser Gly Phe
    210             215             220

Thr Leu Glu Phe Leu Glu His Ala Phe Ser Val Asp Lys Gln Ile Ala
225             230             235             240

Lys Asn Leu Gln Gly Glu Asn Glu Gly Glu Asp Lys Gly Ala Ile Val
            245             250             255

Thr Val Lys Gly Gly Leu Ser Val Ile Lys Pro Pro Thr Asp Glu Gln
            260             265             270

Gln Gln Arg Pro Gln Glu Glu Glu Glu Glu Glu Asp Glu Lys Pro
        275             280             285

Gln Cys Lys Gly Lys Asp Lys His Cys Gln Arg Pro Arg Gly Ser Gln
    290             295             300

Ser Lys Ser Arg Arg Asn Gly Ile Asp Glu Thr Ile Cys Thr Met Arg
305             310             315             320

Leu Arg His Asn Ile Gly Gln Thr Ser Ser Pro Asp Ile Tyr Asn Pro
            325             330             335

Gln Ala Gly Ser Val Thr Thr Ala Thr Ser Leu Asp Phe Pro Ala Leu
            340             345             350

Ser Trp Leu Arg Leu Ser Ala Gly Phe Gly Ser Leu Arg Lys Asn Ala
        355             360             365

Met Phe Val Pro His Tyr Asn Leu Asn Ala Asn Ser Ile Ile Tyr Ala
    370             375             380

Leu Asn Gly Arg Ala Leu Ile Gln Val Val Asn Cys Asn Gly Glu Arg
385             390             395             400

Val Phe Asp Gly Glu Leu Gln Glu Gly Arg Val Leu Ile Val Pro Gln
            405             410             415

Asn Phe Val Val Ala Ala Arg Ser Gln Ser Asp Asn Phe Glu Tyr Val
            420             425             430

Ser Phe Lys Thr Asn Asp Thr Pro Met Ile Gly Thr Leu Ala Gly Ala
        435             440             445

Asn Ser Leu Leu Asn Ala Leu Pro Glu Glu Val Ile Gln His Thr Phe
    450             455             460

Asn Leu Lys Ser Gln Gln Ala Arg Gln Ile Lys Asn Asn Asn Pro Phe
465             470             475             480

Lys Phe Leu Val Pro Pro Gln Glu Ser Gln Lys Arg Ala Val Ala
            485             490             495
```